```
GGAATTCCGT AGTGCGAGGC CGGGCACAGC CTTCCTGTGT GGTTTTACCG CCCAGAGAGC      60
          * **
GTC ATG GAC CTG GGG AAA CCA ATG AAA AGC GTG CTG GTG GTG GCT CTC      108
    Met Asp Leu Gly Lys Pro Met Lys Ser Val Leu Val Val Ala Leu
     1               5                  10                  15

CTT GTC ATT TTC CAG GTA TGC CTG TGT CAA GAT GAG GTC ACG GAC GAT      156
Leu Val Ile Phe Gln Val Cys Leu Cys Gln Asp Glu Val Thr Asp Asp
                  20                  25                  30

TAC ATC GGA GAC AAC ACC ACA GTG GAC TAC ACT TTG TTC GAG TCT TTG      204
Tyr Ile Gly Asp Asn Thr Thr Val Asp Tyr Thr Leu Phe Glu Ser Leu
            35 CHO ### ###      40                  45

TGC TCC AAG AAG GAC GTG CGG AAC TTT AAA GCC TGG TTC CTC CCT ATC      252
Cys Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile
        50                  55                  60

ATG TAC TCC ATC ATT TGT TTC GTG GGC CTA CTG GGC AAT GGG CTG GTC      300
Met Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val
    65                  70                  75

GTG TTG ACC TAT ATC TAT TTC AAG AGG CTC AAG ACC ATG ACC GAT ACC      348
Val Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr
80                  85                  90                  95

TAC CTG CTC AAC CTG GCG GTG GCA GAC ATC CTC TTC CTC CTG ACC CTT      396
Tyr Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu
                100                 105                 110

CCC TTC TGG GCC TAC AGC GCG GCC AAG TCC TGG GTC TTC GGT GTC CAC      444
Pro Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His
          115                 120                 125

TTT TGC AAG CTC ATC TTT GCC ATC TAC AAG ATG AGC TTC TTC AGT GGC      492
Phe Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly
        130                 135                 140

ATG CTC CTA CTT CTT TGC ATC AGC ATT GAC CGC TAC GTG GCC ATC GTC      540
Met Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val
                                == == == == == == == == ==
    145                 150                 155
```

FIG.1A-1

```
CAG GCT GTC TCA GCT CAC CGC CAC CGT GCC CGC GTC CTT CTC ATC AGC      588
Gln Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser
160                 165                 170                 175

AAG CTG TCC TGT GTG GGC AGC GCC ATA CTA GCC ACA GTG CTC TCC ATC      636
Lys Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile
                180                 185                 190

CCA GAG CTC CTG TAC AGT GAC CTC CAG AGG AGC AGC AGT GAG CAA GCG      684
Pro Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala
            195                 200                 205

ATG CGA TGC TCT CTC ATC ACA GAG CAT GTG GAG GCC TTT ATC ACC ATC      732
Met Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile
        210                 215                 220

CAG GTG GCC CAG ATG GTG ATC GGC TTT CTG GTC CCC CTG CTG GCC ATG      780
Gln Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met
    225                 230                 235

AGC TTC TGT TAC CTT GTC ATC ATC CGC ACC CTG CTC CAG GCA CGC AAC      828
Ser Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn
240                 245                 250                 255

TTT GAG CGC AAC AAG GCC ATC AAG GTG ATC ATC GCT GTG GTC GTG GTC      876
Phe Glu Arg Asn Lys Ala Ile Lys Val Ile Ile Ala Val Val Val Val
                260                 265                 270

TTC ATA GTC TTC CAG CTG CCC TAC AAT GGG GTG GTC CTG GCC CAG ACG      924
Phe Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr
            275                 280                 285

GTG GCC AAC TTC AAC ATC ACC AGT AGC ACC TGT GAG CTC AGT AAG CAA      972
Val Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln
        290     CHO ### ### 295                 300

CTC AAC ATC GCC TAC GAC GTC ACC TAC AGC CTG GCC TGC GTC CGC TGC     1020
Leu Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys
    305                 310                 315
```

FIG.1A-2

```
TGC GTC AAC CCT TTC TTG TAC GCC TTC ATC GGC GTC AAG TTC CGC AAC      1068
Cys Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn
320                 325                 330                 335

GAT ATC TTC AAG CTC TTC AAG GAC CTG GGC TGC CTC AGC CAG GAG CAG      1116
Asp Ile Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln
                340                 345                 350

CTC CGG CAG TGG TCT TCC TGT CGG CAC ATC CGG CGC TCC TCC ATG AGT      1164
Leu Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser
            355                 360                 365

GTG GAG GCC GAG ACC ACC ACC ACC TTC TCC CCA TAGGCGACTC TTCTGCCTGG    1217
Val Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro ***
        370                 375

ACTAGAGGGA CCTCTCCCAG GGTCCCTGGG GTGGGGATAG GGAGCAGATG CAATGACTCA    1277

GGACATCCCC CCGCCAAAAG CTGCTCAGGG GAAAAAGCAG CTCTCCCCTC AGAGTGCAAG    1337

CCCCTGCTCC AGAAGATAGC TTCACCCCAA TCCCAGCTAC CTCAACCAAT GCCAAAAAAA    1397

GACAGGGCTG ATAAGCTAAC ACCAGACAGA CAACACTGGG AAACAGAGGC TATTGTCCCC    1457

TAAACCAAAA ACTGAAAGTG AAAGTCCAGA AACTGTTCCC ACCTGCTGGA GTGAAGGGGC    1517

CAAGGAGGGT GAGTGCAAGG GGCGTGGGAG TGGCCTGAAG AGTCCTCTGA ATGAACCTTC    1577

TGGCCTCCCA CAGACTCAAA TGCTCAGACC AGCTCTTCCG AAAACCAGGC CTTATCTCCA    1637

AGACCAGAGA TAGTGGGGAG ACTTCTTGGC TTGGTGAGGA AAAGCGGACA TCAGCTGGTC    1697

AAACAAACTC TCTGAACCCC TCCCTCCATC GTTTTCTTCA CTGTCCTCCA AGCCAGCGGG    1757

AATGGCAGCT GCCACGCCGC CCTAAAAGCA CACTCATCCC CTCACTTGCC GCGTCGCCCT    1817

CCCAGGCTCT CAACAGGGGA GAGTGTGGTG TTTCCTGCAG GCCAGGCCAG CTGCCTCCGC    1877

GTGATCAAAG CCACACTCTG GGCTCCAGAG TGGGGATGAC ATGCACTCAG CTCTTGGCTC    1937
```

FIG.1A–3

CACTGGGATG GGAGGAGAGG ACAAGGGAAA TGTCAGGGGC GGGGAGGGTG ACAGTGGCCG 1997

CCCAAGGCCA CGAGCTTGTT CTTTGTTCTT TGTCACAGGG ACTGAAAACC TCTCCTCATG 2057

TTCTGCTTTC GATTCGTTAA GAGAGCAACA TTTTACCCAC ACACAGATAA AGTTTTCCCT 2117

TGAGGAAACA ACAGCTTTAA AAAAAAAAAA GGAATTC 2154

FIG.1A-4

```
GGAATTCCCT GATATACACC TGGACCACCA CCA ATG GAT ATA CAA ATG GCA AAC 54
          * **
                                     Met Asp Ile Gln Met Ala Asn
                                      1               5

AAT TTT ACT CCG CCC TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC 102
Asn Phe Thr Pro Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu
CHO ### ###
          10                  15                  20

TAT GCA CAT CAC AGC ACG GCC AGG ATA GTA ATG CCT CTG CAT TAC AGC 150
Tyr Ala His His Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser
      25                  30                  35

CTC GTC TTC ATC ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC 198
Leu Val Phe Ile Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val
 40                  45                  50                  55

ATT GTT CAA AAC AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA 246
Ile Val Gln Asn Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr
                    60                  65                  70

AAT TTG GTG ATT TCT GAT ATA CTT TTT ACC ACG GCT TTG CCT ACA CGA 294
Asn Leu Val Ile Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg
               75                  80                  85

ATA GCC TAC TAT GCA ATG GGC TTT GAC TGG AGA ATC GGA GAT GCC TTG 342
Ile Ala Tyr Tyr Ala Met Gly Phe Asp Trp Arg Ile Gly Asp Ala Leu
          90                  95                  100

TGT AGG ATA ACT GCG CTA GTG TTT TAC ATC AAC ACA TAT GCA GGT GTG 390
Cys Arg Ile Thr Ala Leu Val Phe Tyr Ile Asn Thr Tyr Ala Gly Val
     105                 110                 115
```

FIG.1B-1

```
AAC TTT ATG ACC TGC CTG AGT ATT GAC CGC TTC ATT GCT GTG GTG CAC 438
Asn Phe Met Thr Cys Leu Ser Ile Asp Arg Phe Ile Ala Val Val His
120                 125                 130                 135
CCT CTA CGC TAC AAC AAG ATA AAA AGG ATT GAA CAT GCA AAA GGC GTG 486
Pro Leu Arg Tyr Asn Lys Ile Lys Arg Ile Glu His Ala Lys Gly Val
                140                 145                 150
TGC ATA TTT GTC TGG ATT CTA GTA TTT GCT CAG ACA CTC CCA CTC CTC 534
Cys Ile Phe Val Trp Ile Leu Val Phe Ala Gln Thr Leu Pro Leu Leu
            155                 160                 165
ATC AAC CCT ATG TCA AAG CAG GAG GCT GAA AGG ATT ACA TGC ATG GAG 582
Ile Asn Pro Met Ser Lys Gln Glu Ala Glu Arg Ile Thr Cys Met Glu
        170                 175                 180
TAT CCA AAC TTT GAA GAA ACT AAA TCT CTT CCC TGG ATT CTG CTT GGG 630
Tyr Pro Asn Phe Glu Glu Thr Lys Ser Leu Pro Trp Ile Leu Leu Gly
    185                 190                 195
GCA TGT TTC ATA GGA TAT GTA CTT CCA CTT ATA ATC ATT CTC ATC TGC 678
Ala Cys Phe Ile Gly Tyr Val Leu Pro Leu Ile Ile Ile Leu Ile Cys
200                 205                 210                 215
TAT TCT CAG ATC TGC TGC AAA CTC TTC AGA ACT GCC AAA CAA AAC CCA 726
Tyr Ser Gln Ile Cys Cys Lys Leu Phe Arg Thr Ala Lys Gln Asn Pro
                220                 225                 230
CTC ACT GAG AAA TCT GGT GTA AAC AAA AAG GCT CTC AAC ACA ATT ATT 774
Leu Thr Glu Lys Ser Gly Val Asn Lys Lys Ala Leu Asn Thr Ile Ile
            235                 240                 245
CTT ATT ATT GTT GTG TTT GTT CTC TGT TTC ACA CCT TAC CAT GTT GCA 822
Leu Ile Ile Val Val Phe Val Leu Cys Phe Thr Pro Tyr His Val Ala
        250                 255                 260
```

FIG.1B–2

```
ATT ATT CAA CAT ATG ATT AAG AAG CTT CGT TTC TCT AAT TTC CTG GAA   870

Ile Ile Gln His Met Ile Lys Lys Leu Arg Phe Ser Asn Phe Leu Glu
    265                 270                 275

TGT AGC CAA AGA CAT TCG TTC CAG ATT TCT CTG CAC TTT ACA GTA TGC   918

Cys Ser Gln Arg His Ser Phe Gln Ile Ser Leu His Phe Thr Val Cys
280                 285                 290                 295

CTG ATG AAC TTC AAT TGC TGC ATG GAC CCT TTT ATC TAC TTC TTT GCA   966

Leu Met Asn Phe Asn Cys Cys Met Asp Pro Phe Ile Tyr Phe Phe Ala
                300                 305                 310

TGT AAA GGG TAT AAG AGA AAG GTT ATG AGG ATG CTG AAA CGG CAA GTC  1014

Cys Lys Gly Tyr Lys Arg Lys Val Met Arg Met Leu Lys Arg Gln Val
            315                 320                 325

AGT GTA TCG ATT TCT AGT GCT GTG AAG TCA GCC CCT GAA GAA AAT TCA  1062

Ser Val Ser Ile Ser Ser Ala Val Lys Ser Ala Pro Glu Glu Asn Ser
        330                 335                 340

CGT GAA ATG ACA GAA ACG CAG ATG ATG ATA CAT TCC AAG TCT TCA AAT  1110

Arg Glu Met Thr Glu Thr Gln Met Met Ile His Ser Lys Ser Ser Asn
    345                 350                 355

GGA AAG TGAAATGGAT TGTATTTTGG TTTATAGTGA CGTAAACTGT ATGACAAACT  1166

Gly Lys ***
360

TTGCAGGACT TCCCTTATAA AGCAAAATAA TTGTTCAGCT TCCAATTAGT ATTCTTTTAT 1226

ATTTCTTTCA TTGGGCGCTT TCCCATCTCC AACTCGGAAG TAAGCCCAAG AGAACAACAT 1286

AAAGCAAACA ACATAAAGCA CAATAAAAAT GCAAATAAAT ATTTTCATTT TTATTTGTAA 1346
```

FIG.1B-3

ACGAATACAC CAAAAGGAGG CGCTCTTAAT AACTCCCAAT GTAAAAAGTT TTGTTTTAAT 1406

AAAAAATTAA TTATTATTCT TGCCAACAAA TGGCTAGAAA GGACTGAATA GATTATATAT 1466

TGCCAGATGT TAATACTGTA ACATACTTTT TAAATAACAT ATTTCTTAAA TCCAAATTTC 1526

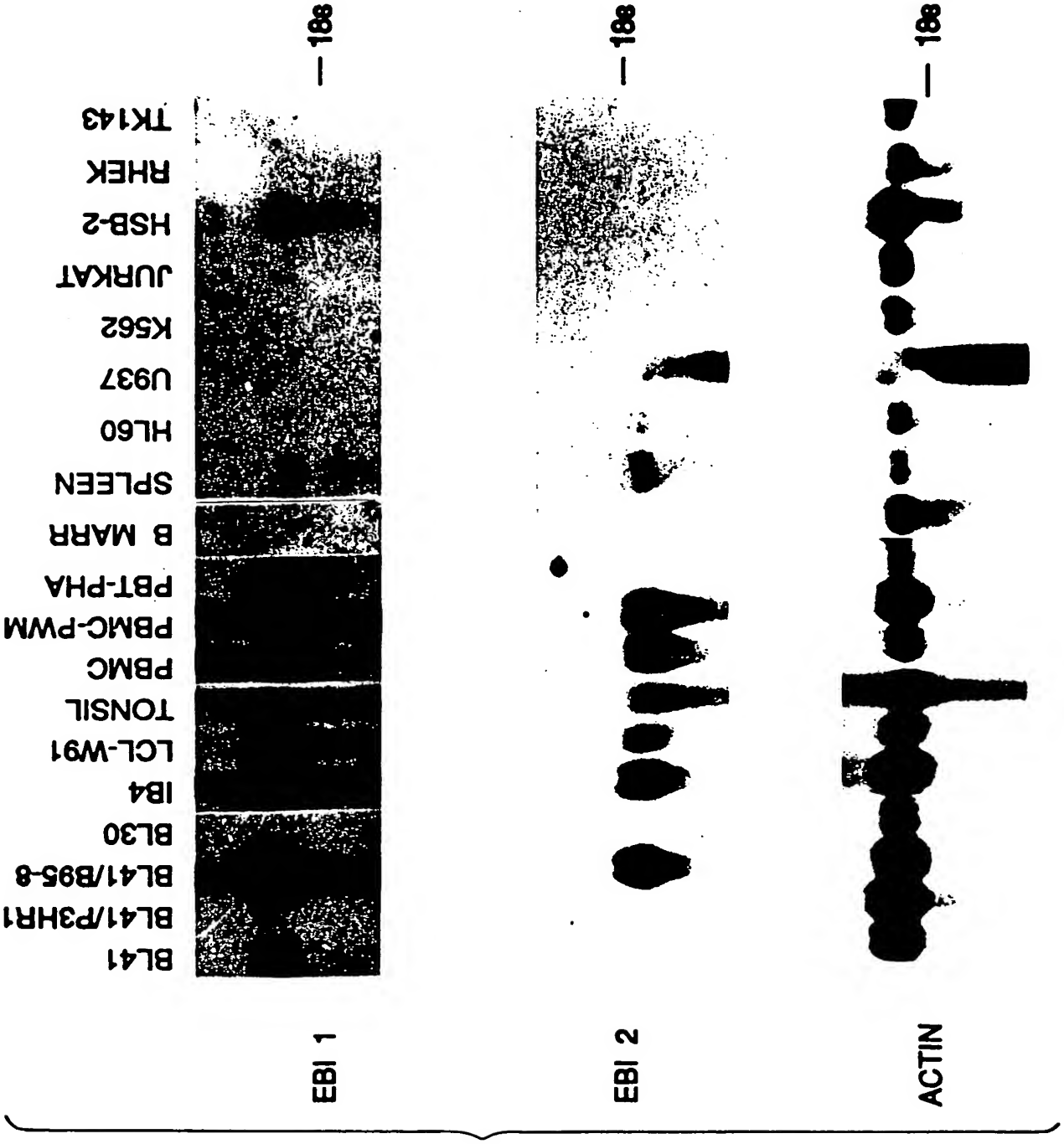
TCTCAATGTT AGATTTAATT CCCTCAATAA CACCAATGTT TTGTTTTGTT TCGTTCTGGG 1586

TCATAAAACT TTGTTAAGGA ACTCTTTTGG AATAAAGAGC AGGATGCTGC GGAATTC 1643

FIG.1B-4


28s
18s
L C B B E L L L
ACTIN
CD44
CATHEPSIN H
p68
MARCKS
SERGLYCIN
EBI 1
EBI 2

FIG. 2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18s
18s
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HSB-2
JURKAT
K562
U937
HL60
SPLEEN
B MARR
PBT-PHA
PBMC-PWM
PBMC
TONSIL
LCL-W91
IB4
BL30
BL41/B95-8
BL41/P3HR1
BL41
EBI 1
EBI 2
ACTIN

FIG. 3

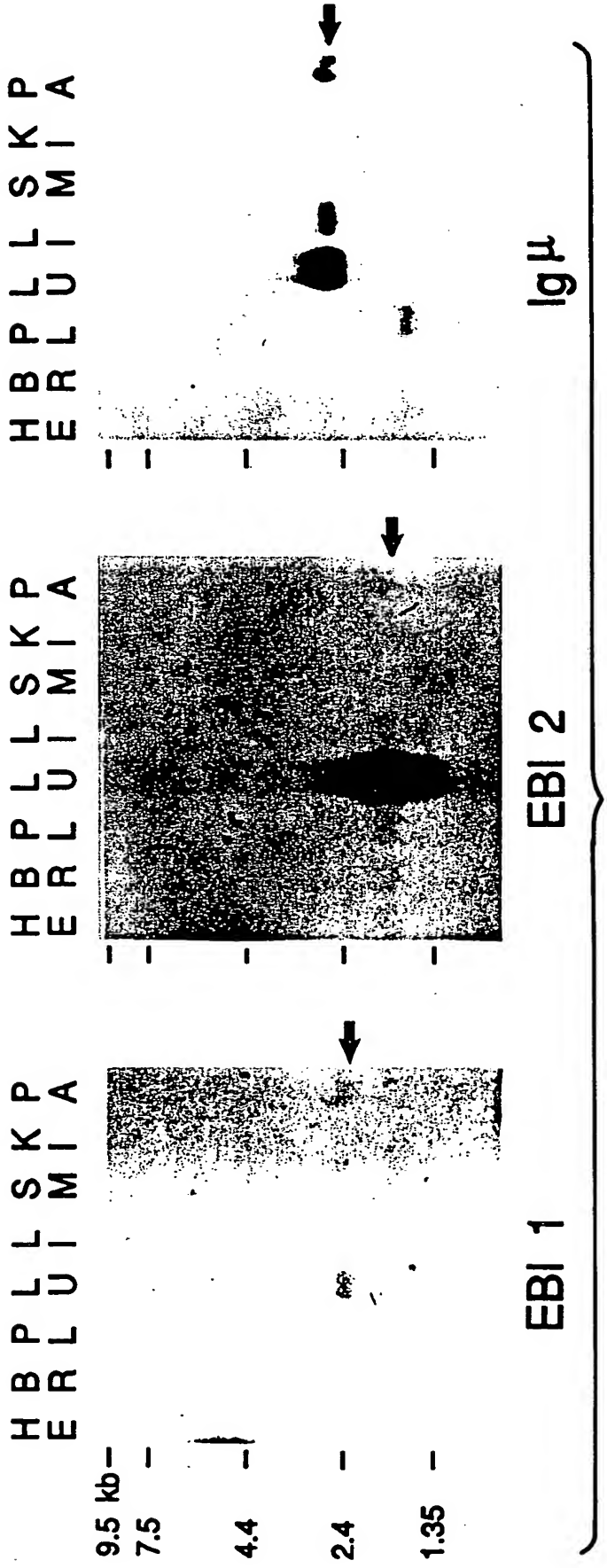
HBPLLSKP
ERLUIMIA
Igμ
HBPLLSKP
ERLUIMIA
EBI 2
HBPLLSKP
ERLUIMIA
EBI 1
9.5 kb
7.5
4.4
2.4
1.35

FIG. 4

```
GAATTCCGCA GCC ATG ACC CCG CAG CTT CTC CTG GCC CTT GTC CTC TGG    49

                  Met Thr Pro Gln Leu Leu Leu Ala Leu Val Leu Trp
                   1               5                  10

GCC AGC TGC CCG CCC TGC AGT GGA AGG AAA GGG CCC CCA GCA GCT CTG   97

Ala Ser Cys Pro Pro Cys Ser Gly Arg Lys Gly Pro Pro Ala Ala Leu
         15                  20                  25

ACA CTG CCC CGG GTG CAA TGC CGA GCC TCT CGG TAC CCG ATC GCC GTG  145

Thr Leu Pro Arg Val Gln Cys Arg Ala Ser Arg Tyr Pro Ile Ala Val
     30                  35                  40

GAT TGC TCC TGG ACC CTG CCG CCT GCT CCA AAC TCC ACC AGC CCC GTG  193

Asp Cys Ser Trp Thr Leu Pro Pro Ala Pro Asn Ser Thr Ser Pro Val
 45                  50                  CHO ### ###         60
                                         55

TCC TTC ATT GCC ACG TAC AGG CTC GGC ATG GCT GCC CGG GGC CAC AGC  241

Ser Phe Ile Ala Thr Tyr Arg Leu Gly Met Ala Ala Arg Gly His Ser
                 65                  70                  75

TGG CCC TGC CTG CAG CAG ACG CCA ACG TCC ACC AGC TGC ACC ATC AGC  289

Trp Pro Cys Leu Gln Gln Thr Pro Thr Ser Thr Ser Cys Thr Ile Thr
             80                  85                  90

GAT GTC CAG CTG TTC TCC ATG GCT CCC TAC GTG CTC AAT GTC ACC GCC  337

Asp Val Gln Leu Phe Ser Met Ala Pro Tyr Val Leu Asn Val Thr Ala
         95                  100                 105 CHO ### ###

GTC CAC CCC TGG GGC TCC AGC AGC AGC TTC GTG CCT TTC ATA ACA GAG  385

Val His Pro Trp Gly Ser Ser Ser Ser Phe Val Pro Phe Ile Thr Glu
     110                 115                 120

CAC ATC ATC AAG CCC GAC CCT CCA GAA GGC GTG CGC CTA AGC CCC CTC  433

His Ile Ile Lys Pro Asp Pro Pro Glu Gly Val Arg Leu Ser Pro Leu
125                 130                 135                 140
```

FIG.5A

```
GCT GAG CGC CAC GTA CAG GTG CAG TGG GAG CCT CCC GGG TCC TGG CCC     481

Ala Glu Arg His Val Gln Val Gln Trp Glu Pro Pro Gly Ser Trp Pro
                145                 150                 155

TTC CCA GAG ATC TTC TCA CTG AAG TAC TGG ATC CGT TAC AAG CGT GAG     529

Phe Pro Glu Ile Phe Ser Leu Lys Tyr Trp Ile Arg Tyr Lys Arg Gln
            160                 165                 170

GGA GCT GCG CGC TTC CAC CGG GTG GGG CCC ATT GAA GCC ACG TCC TTC     577

Gly Ala Ala Arg Phe His Arg Val Gly Pro Ile Glu Ala Thr Ser Phe
        175                 180                 185

ATC CTC AGG GCT GTG CGG CCC CGA GCC AGG TAC TAC GTC CAA GTG GCG     625

Ile Leu Arg Ala Val Arg Pro Arg Ala Arg Tyr Tyr Val Gln Val Ala
    190                 195                 200

GCT CAG GAC CTC ACA GAC TAC GGG GAA CTG AGT GAC TGG AGT CTC CCC     673

Ala Gln Asp Leu Thr Asp Tyr Gly Glu Leu Ser Asp Trp Ser Leu Pro
205                 210                 215                 220

GCC ACT GCC ACA ATG AGC CTG GGC AAG TAGCAAGGGC TTCCCGCTGC          720

Ala Thr Ala Thr Met Ser Leu Gly Lys ***
                225

CTCCAGACAG CACCTGGGTC CTCGCCACCC TAAGCCCCGG GACACCTGTT GGAGGGCGGA  780

TGGGATCTGC CTAGCCTGGG CTGGAGTCCT TGCTTTGCTG CTGCTGAGCT GCCGGGCAAC  840

CTCAGATGAC CGACTTTTCC CTTTGAGCCT CAGTTTCTCT AGCTGAGAAA TGGAGATGTA  900

CTACTCTCTC CTTTACCTTT ACCTTTACCA CAGTGCAGGG CTGACTGAAC TGTCACTGTG  960
```

FIG.5B

AGATATTTTT TATTGTTTAA TTAGAAAAGA ATTGTTGTTG GGCTGGGCGC AGTGGATCGC 1020

ACCTGTAATC CCAGTCACTG GGAAGCCGAC GTGGGTGGGT AGCTTGAGGC CAGGAGCTCG 1080

AAACCAGTCC GGGCCACACA GCAAGACCCC ATCTCTAAAA AATTAATATA AATATAAAAT 1140

AAAAAAAAAA AAAAGGAATT C 1161

FIG.5C

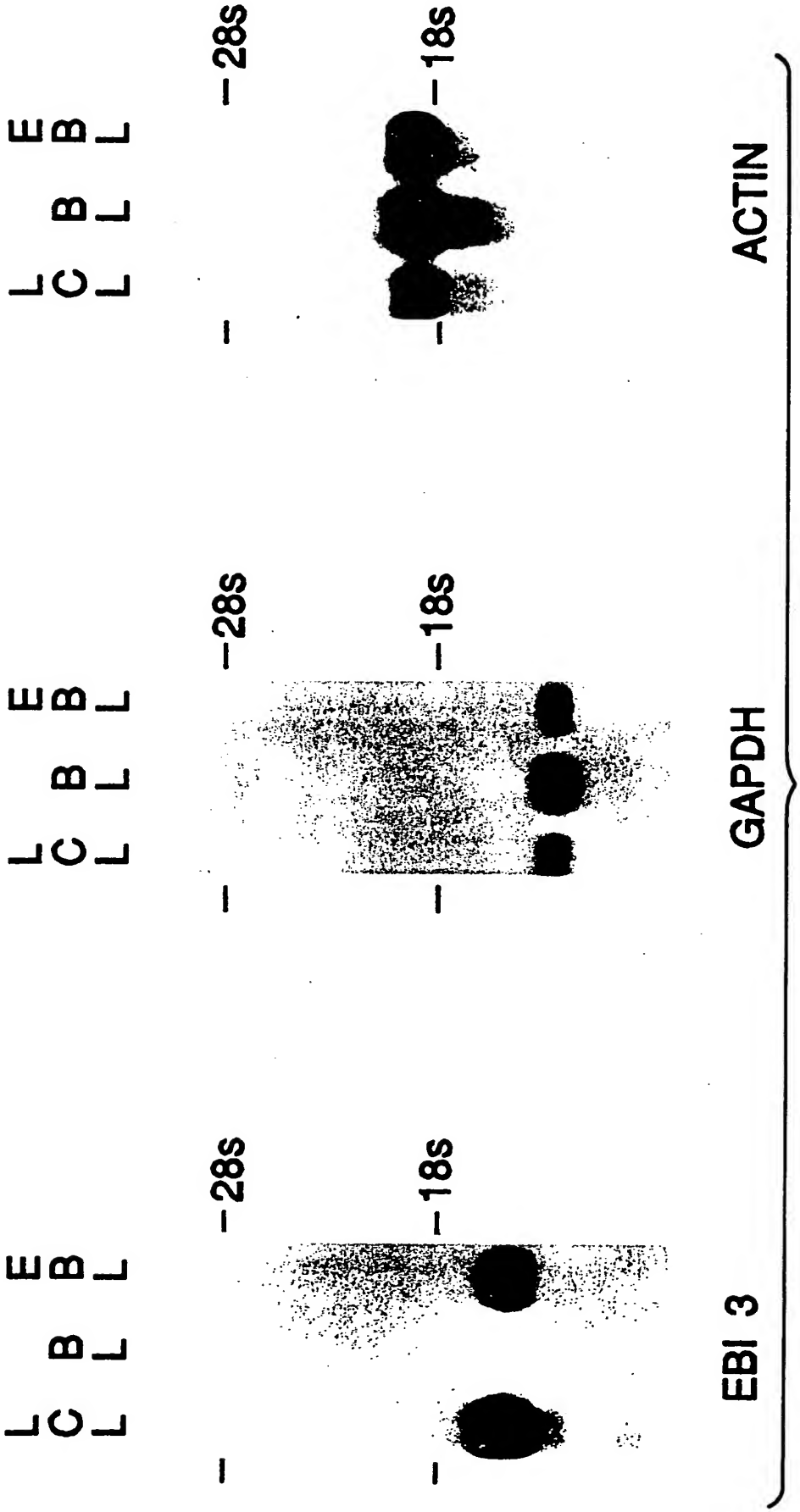

FIG. 6

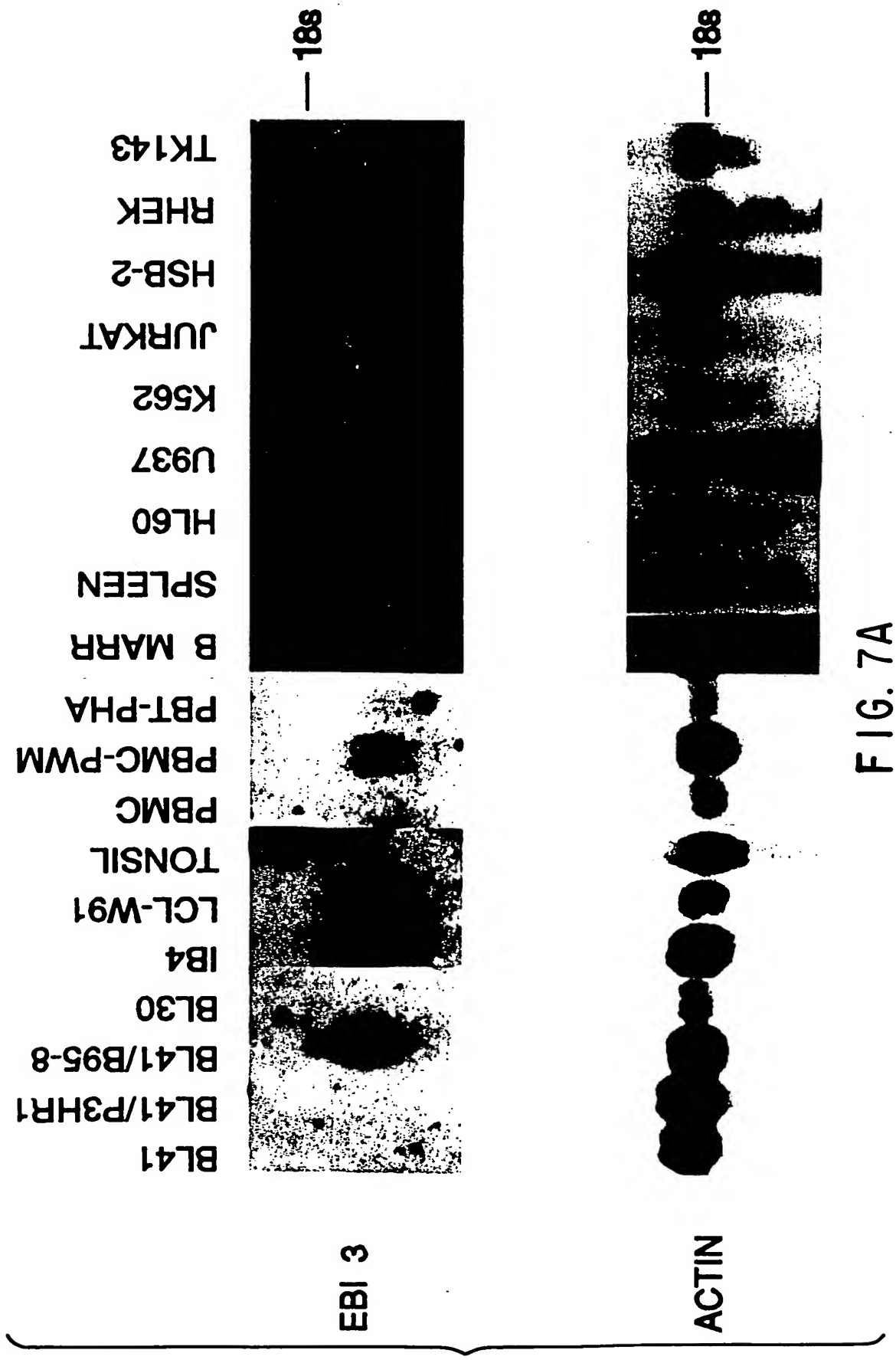
18s
18s
TK143
RHEK
HSB-2
JURKAT
K562
U937
HL60
SPLEEN
B MARR
PBT-PHA
PBMC-PWM
PBMC
TONSIL
LCL-W91
IB4
BL30
BL41/B95-8
BL41/P3HR1
BL41
EBI 3
ACTIN

FIG. 7A

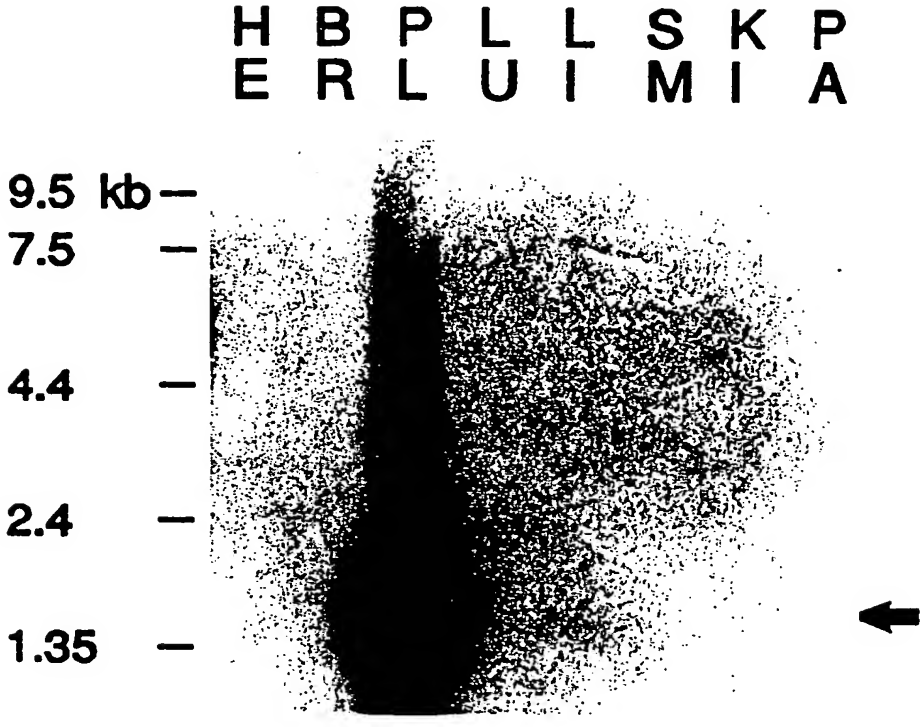

FIG. 7B